

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Ashkenazi, Avi J.
Baker, Kevin
Chuntharapai, Anan
Gurney, Austin
Kim, Kyung Jin
Wood, William

(ii) TITLE OF INVENTION: Apo-2DcR

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 12-Jun-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/049911

(B) FILING DATE: 18-JUN-1997

(viii) ATTORNEY/AGENT INFORMATION:

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(A) NAME: Marschang, Diane L.

(B) REGISTRATION NUMBER: 35,600

(C) REFERENCE/DOCKET NUMBER: P1110P1

(ix) TELECOMMUNICATION INFORMATION:

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(A) TELEPHONE: 650/225-5416

(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val
1 5 10 15

Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg
20 25 30

Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
35 40 45

30 His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser
50 55 60

Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
65 70 75

35

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Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val
80 85 90

Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
5 95 100 105

Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn
110 115 120

Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
10 125 130 135

Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val
140 145 150

Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu
155 160 165

Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
170 175 180

Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
185 190 195

Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
200 205 210

Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
215 220 225

Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr
230 235 240

Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu
35 245 250 255

Ile Val Phe Val

259

(2) INFORMATION FOR SEQ ID NO:2:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1180 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

10

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

15 GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50

ATTTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC 100

CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC 150

AGGGTGCGAC CCAGGACCCA GGACGGCGTC GGGAACCATA CC ATG 195

Met

1

25 GCC CGG ATC CCC AAG ACC CTA AAG TTC GTC GTC GTC ATC 234

Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile

5

10

GTC GCG GTC CTG CTG CCA GTC CTA GCT TAC TCT GCC ACC 273

30 Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr

15

20

25

ACT GCC CGG CAG GAG GAA GTT CCC CAG CAG ACA GTG GCC 312

Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala

35

30

35

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CCA CAG CAA CAG AGG CAC AGC TTC AAG GGG GAG GAG TGT 351
 Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys
 45 50

5 CCA GCA GGA TCT CAT AGA TCA GAA CAT ACT GGA GCC TGT 390
 Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys
 55 60 65

10 AAC CCG TGC ACA GAG GGT GTG GAT TAC ACC AAC GCT TCC 429
 Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser
 70 75

AAC AAT GAA CCT TCT TGC TTC CCA TGT ACA GTT TGT AAA 468
 Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys
 80 85 90

TCA GAT CAA AAA CAT AAA AGT TCC TGC ACC ATG ACC AGA 507
 Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
 95 100 105

GAC ACA GTG TGT CAG TGT AAA GAA GGC ACC TTC CGG AAT 546
 Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn
 110 115

25 GAA AAC TCC CCA GAG ATG TGC CGG AAG TGT AGC AGG TGC 585
 Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys
 120 125 130

30 CCT AGT GGG GAA GTC CAA GTC AGT AAT TGT ACG TCC TGG 624
 Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp
 135 140

35 GAT GAT ATC CAG TGT GTT GAA GAA TTT GGT GCC AAT GCC 663
 Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala
 145 150 155

05.09.2020 12:00:00

ACT GTG GAA ACC CCA GCT GCT GAA GAG ACA ATG AAC ACC 702
Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn' Thr
160 165 170

5 AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG 741
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
175 180

10 AAC ACC AGC CCA GGG ACT CCT GCC CCA GCT GCT GAA GAG 780
Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
185 190 195

ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT 819
Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala
200 205

GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA 858
Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro
210 215 220

GCT GCT GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT 897
Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro
225 230 235

25 GCC TCT TCT CAT TAC CTC TCA TGC ACC ATC GTA GGG ATC 936
Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
240 245

30 ATA GTT CTA ATT GTG CTT CTG ATT GTG TTT GTT T 970
Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
250 255 259

GAAAGACTTC ACTGTGGAAG AAATTCCTTC CTTACCTGAA AGGTTTCAGGT 1020

35 AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCTCCC 1070

TCTGCTGTGT TCCCACAGAC AGAAACGCCT GCCCCTGCCC CAAAAAAAAA 1120

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1170

5 AAAAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly
-40 -35 -30

Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro
-25 -20 -15

Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
-10 -5 1 5

Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro
10 15 20

Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro
25 30 35

Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe Lys Gly
40 45 50

Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala
55 60 65

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Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
70 75 80

Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
85 90 95

Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
100 105 110

Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys
115 120 125

Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn
130 135 140

Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala
145 150 155

Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
160 165 170

Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr
175 180 185

Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
190 195 200

Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
205 210 215

Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
220 225 230

Ser Pro Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile
235 240 245

Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
250 255 259

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1180 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50

ATTTTGGGA GTTTGACCAG AG ATG CAA GGG GTG AAG GAG 90

Met Gln Gly Val Lys Glu

-40

-35

CGC TTC CTA CCG TTA GGG AAC TCT GGG GAC AGA GCG CCC 129

Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp Arg Ala Pro

-30

-25

CGG CCG CCT GAT GGC CGA GGC AGG GTG CGA CCC AGG ACC 168

Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr

-20

-15

-10

CAG GAC GGC GTC GGG AAC CAT ACC ATG GCC CGG ATC CCC 207

Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro

-5

1

5

AAG ACC CTA AAG TTC GTC GTC GTC ATC GTC GCG GTC CTG 246

Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu

10

15

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CTG CCA GTC CTA GCT TAC TCT GCC ACC ACT GCC CGG CAG 285
 Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln
 20 25 30

5 GAG GAA GTT CCC CAG CAG ACA GTG GCC CCA CAG CAA CAG 324
 Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln
 35 40

10 AGG CAC AGC TTC AAG GGG GAG GAG TGT CCA GCA GGA TCT 363
 Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser
 45 50 55

CAT AGA TCA GAA CAT ACT GGA GCC TGT AAC CCG TGC ACA 402
 His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr
 60 65 70

GAG GGT GTG GAT TAC ACC AAC GCT TCC AAC AAT GAA CCT 441
 Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro
 75 80

TCT TGC TTC CCA TGT ACA GTT TGT AAA TCA GAT CAA AAA 480
 Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys
 85 90 95

25 CAT AAA AGT TCC TGC ACC ATG ACC AGA GAC ACA GTG TGT 519
 His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys
 100 105

30 CAG TGT AAA GAA GGC ACC TTC CGG AAT GAA AAC TCC CCA 558
 Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro
 110 115 120

35 GAG ATG TGC CGG AAG TGT AGC AGG TGC CCT AGT GGG GAA 597
 Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
 125 130 135

GTC CAA GTC AGT AAT TGT ACG TCC TGG GAT GAT ATC CAG 636
 Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln
 140 145

5 TGT GTT GAA GAA TTT GGT GCC AAT GCC ACT GTG GAA ACC 675
 Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr
 150 155 160

10 CCA GCT GCT GAA GAG ACA ATG AAC ACC AGC CCG GGG ACT 714
 Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr
 165 170

CCT GCC CCA GCT GCT GAA GAG ACA ATG AAC ACC AGC CCA 753
 Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro
 175 180 185

GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG ACC ACC 792
 Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
 190 195 200

AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG 831
 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
 205 210

ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG 870
 Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
 215 220 225

30 ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC TCT TCT CAT 909
 Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His
 230 235

35 TAC CTC TCA TGC ACC ATC GTA GGG ATC ATA GTT CTA ATT 948
 Tyr Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile
 240 245 250

GTG CTT CTG ATT GTG TTT GTT T GAAAGACTTC ACTGTGGAAG 990
Val Leu Leu Ile Val Phe Val
255 259

5 AAATTCCTTC CTTACCTGAA AGGTTTCAGGT AGGCGCTGGC TGAGGGCGGG 1040
GGGCGCTGGA CACTCTCTGC CCTGCCTCCC TCTGCTGTGT TCCCACAGAC 1090
AGAAACGCCT GCCCCTGCCC CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140
10 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTAAAACGA CGGCCAGTTA AATAGACCTG CAATTATTAA TCT 43

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAGGAAACAG CTATGACCAC CTGCACACCT GCAAATCCAT T 41

(2) INFORMATION FOR SEQ ID NO:7:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His
1 5 10 15
Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly
20 25 30
Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys
35 40 45
Gly Cys Arg Lys
49

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
1 5 10 15

Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
 20 25 30

Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
 5 35 40 45

Cys Lys Glu
 48

10 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50

GCTAAAGCTG AGGCAGCGGG 70

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1799 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

35

CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50

GCGCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC 100

5 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145

Met Glu

1

CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184

10 Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg

5

10

15

AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala

20

25

AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262

Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val

30

35

40

GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301

Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala

45

50

25 CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340

Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala

55

60

65

GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379

30 Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu

70

75

80

TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418

Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp

35

85

90

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TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC 457
Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His
95 100 105

5 TGG AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT 496
Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys
110 115

10 GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACG ACC 535
Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr
120 125 130

AGA AAC ACA GTG TGT CAG TGC GAA GAA GGC ACC TTC CGG 574
Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg
135 140 145

GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA 613
Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr
150 155

GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA 652
Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr
160 165 170

25 CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC 691
Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly
175 180

30 ATC ATC ATA GGA GTC ACA GTT GCA GCC GTA GTC TTG ATT 730
Ile Ile Ile Gly Val Thr Val Ala Ala Val Val Leu Ile
185 190 195

35 GTG GCT GTG TTT GTT TGC AAG TCT TTA CTG TGG AAG AAA 769
Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
200 205 210

CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159
 Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys
 330 335 340

5 GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198
 Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
 345 350

10 TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237
 Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
 355 360 365

GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276
 Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
 370 375

CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315
 Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His
 380 385 390

TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354
 Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
 395 400 405

25 GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400
 Ala Asp Ser Ala Xaa Ser
 410 411

CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450

AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500

CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACCTT TTTACTGCAC 1550

35 TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

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GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA 1650

TTGTTTTTCAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700

5 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAG 1750

GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:11:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
1 5 10 15

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
20 25 30

Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
35 40 45

Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
50 55 60

30 Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser
65 70 75

Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp
80 85 90

35

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	Gly	Arg	Asp	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr
					95					100					105
5	His	Trp	Asn	Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp
					110					115					120
	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	Arg	Asn	Thr
					125					130					135
10	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	Glu	Glu	Asp	Ser	Pro
					140					145					150
	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly	Met	Val
					155					160					165
	Lys	Val	Gly	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His
					170					175					180
	Lys	Glu	Ser	Gly	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val
20					185					190					195
	Leu	Ile	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys
					200					205					210
25	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly	Asp
					215					220					225
	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	Gly	Ala	Glu	Asp
					230					235					240
30	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	Leu	Gln	Pro	Thr	Gln	Val
					245					250					255
	Pro	Glu	Gln	Glu	Met	Glu	Val	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly
35					260					265					270

05096500061299

Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro
275 280 285

Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala
290 295 300

Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp
305 310 315

Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg
320 325 330

Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu
335 340 345

Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp
350 355 360

Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
365 370 375

Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
380 385 390

Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
395 400 405

Ala Asp Ser Ala Xaa Ser
410 411

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: Nucleic Acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:13:

10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

040965002061298